*FIG. 1*

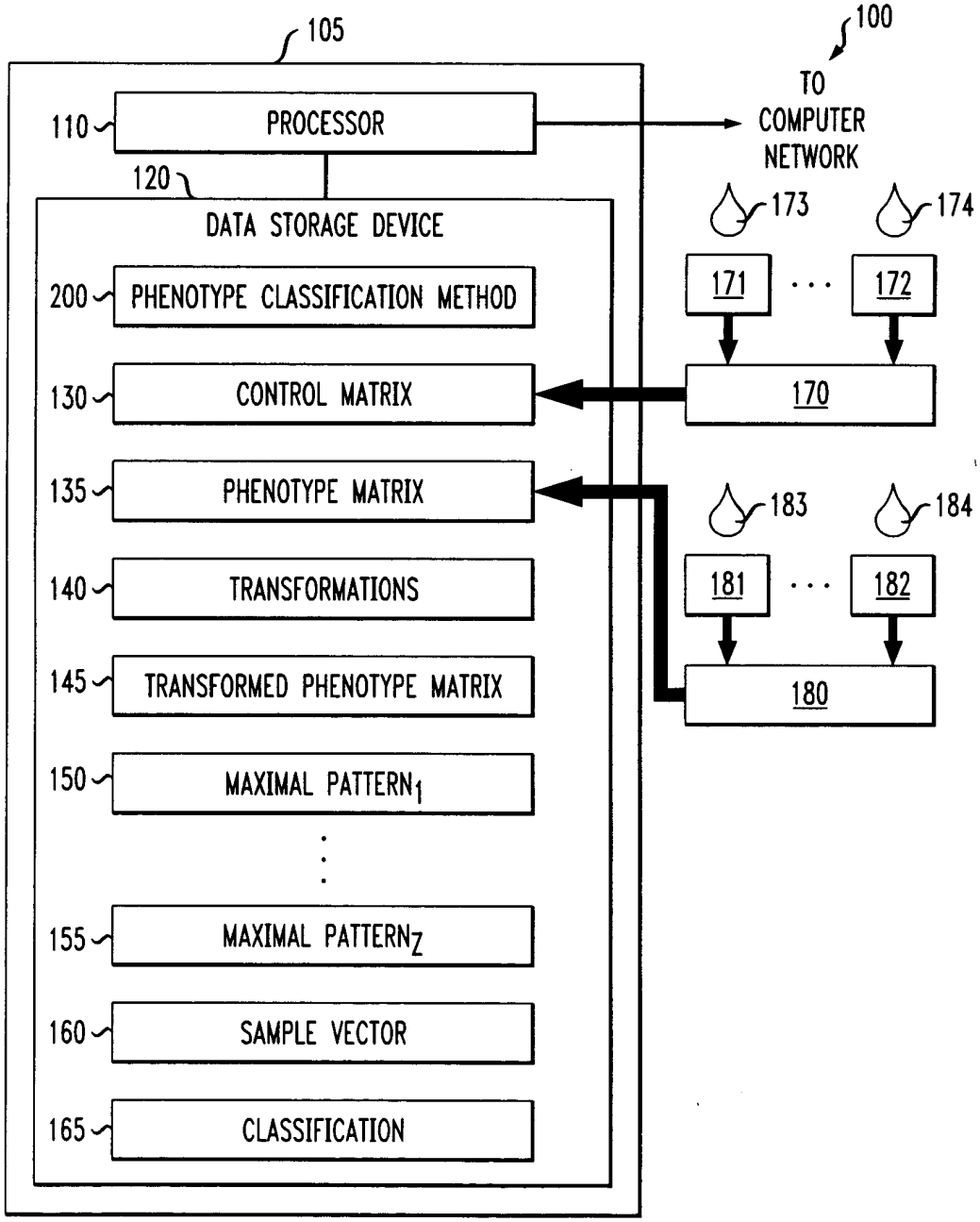

105
100
TO
COMPUTER
NETWORK
110
PROCESSOR
120
DATA STORAGE DEVICE
173
174
171
172
200
PHENOTYPE CLASSIFICATION METHOD
130
CONTROL MATRIX
170
135
PHENOTYPE MATRIX
183
184
181
182
140
TRANSFORMATIONS
145
TRANSFORMED PHENOTYPE MATRIX
180
150
MAXIMAL PATTERN1
155
MAXIMAL PATTERNZ
160
SAMPLE VECTOR
165
CLASSIFICATION

*FIG. 2*

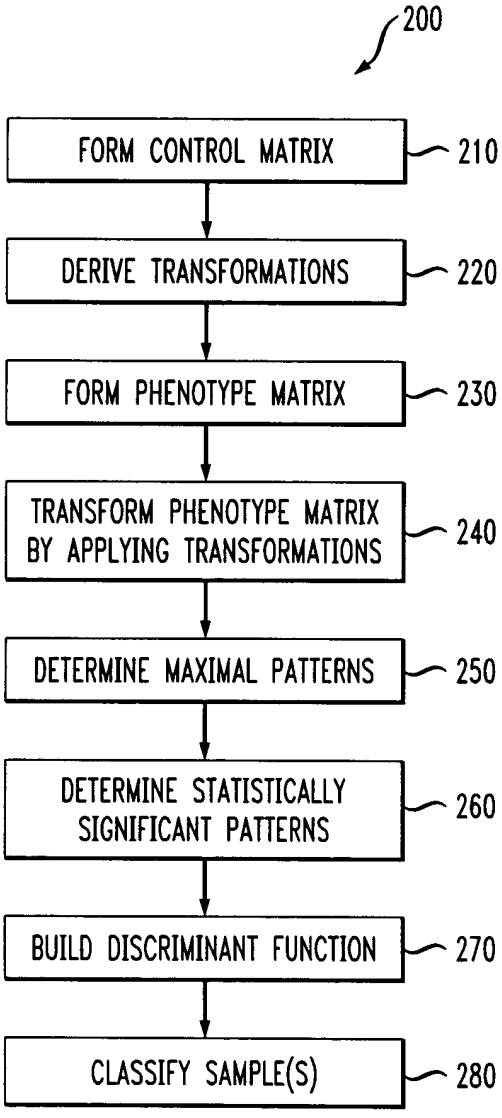

200
FORM CONTROL MATRIX
210
DERIVE TRANSFORMATIONS
220
FORM PHENOTYPE MATRIX
230
TRANSFORM PHENOTYPE MATRIX BY APPLYING TRANSFORMATIONS
240
DETERMINE MAXIMAL PATTERNS
250
DETERMINE STATISTICALLY SIGNIFICANT PATTERNS
260
BUILD DISCRIMINANT FUNCTION
270
CLASSIFY SAMPLE(S)
280

*FIG. 3*

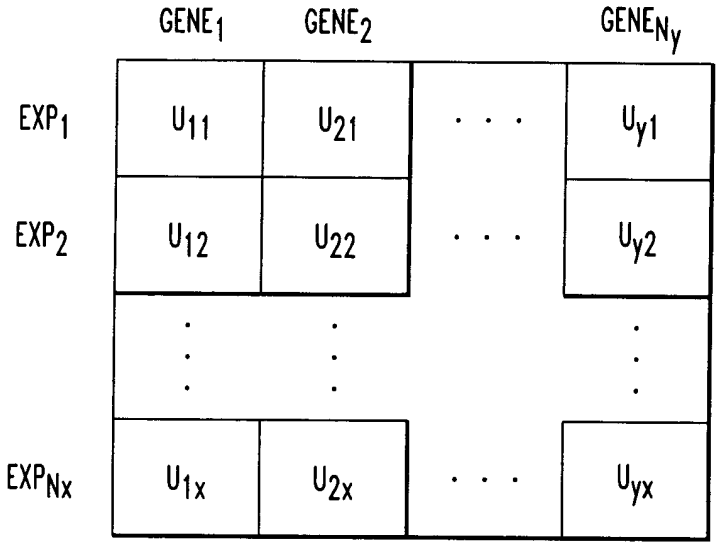

GENE1
GENE2
GENENy
EXP1
EXP2
EXPNx
U11
U21
Uy1
U12
U22
Uy2
U1x
U2x
Uyx

*FIG. 4*

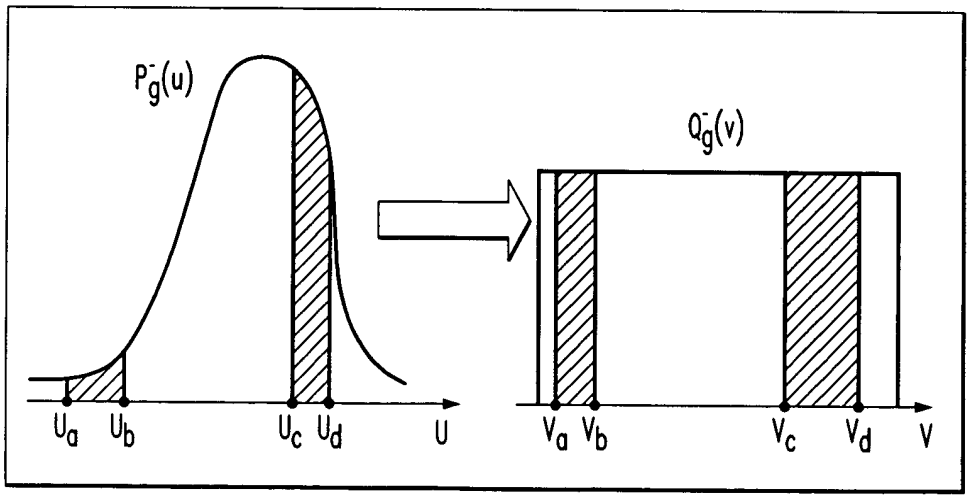

P-g(u)
Q-g(v)
Ua
Ub
Uc
Ud
U
Va
Vb
Vc
Vd
V

*FIG. 5*

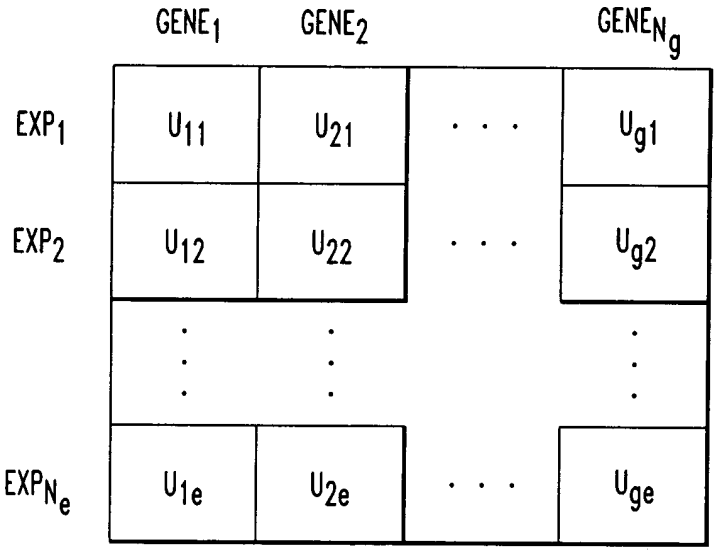

GENE1
GENE2
GENENg
EXP1
EXP2
EXPNe
U11
U21
Ug1
U12
U22
Ug2
U1e
U2e
Uge

*FIG. 6*

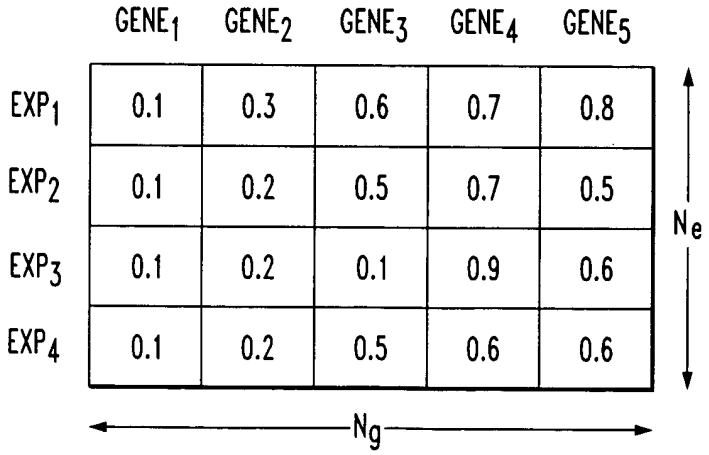
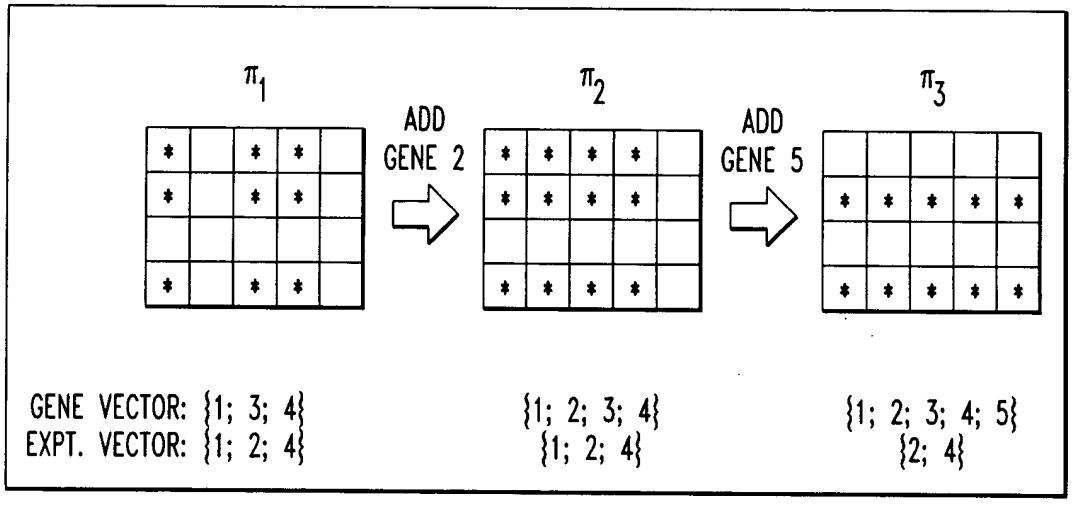

GENE1
GENE2
GENE3
GENE4
GENE5
EXP1
EXP2
EXP3
EXP4
0.1 0.3 0.6 0.7 0.8
0.1 0.2 0.5 0.7 0.5
0.1 0.2 0.1 0.9 0.6
0.1 0.2 0.5 0.6 0.6
Ne
Ng

*FIG. 7*

$$V_{G,E} = \begin{bmatrix} 0.1 & 0.6 & 0.7 \\ 0.1 & 0.5 & 0.7 \\ 0.1 & 0.5 & 0.6 \end{bmatrix}$$

*FIG. 8*



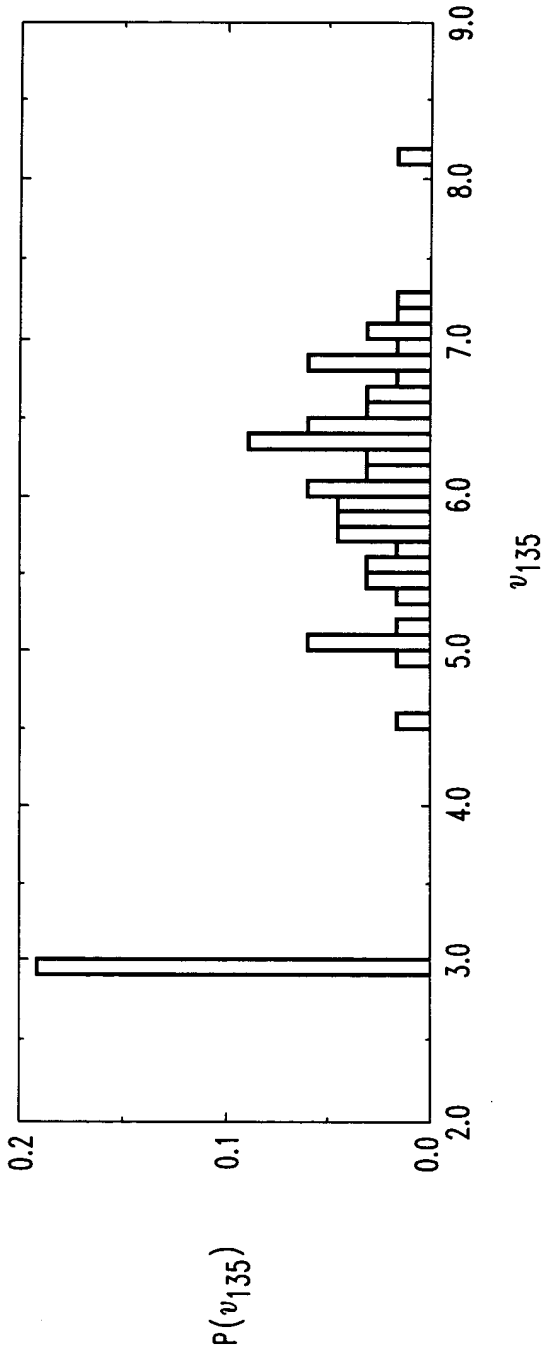



*FIG. 9*

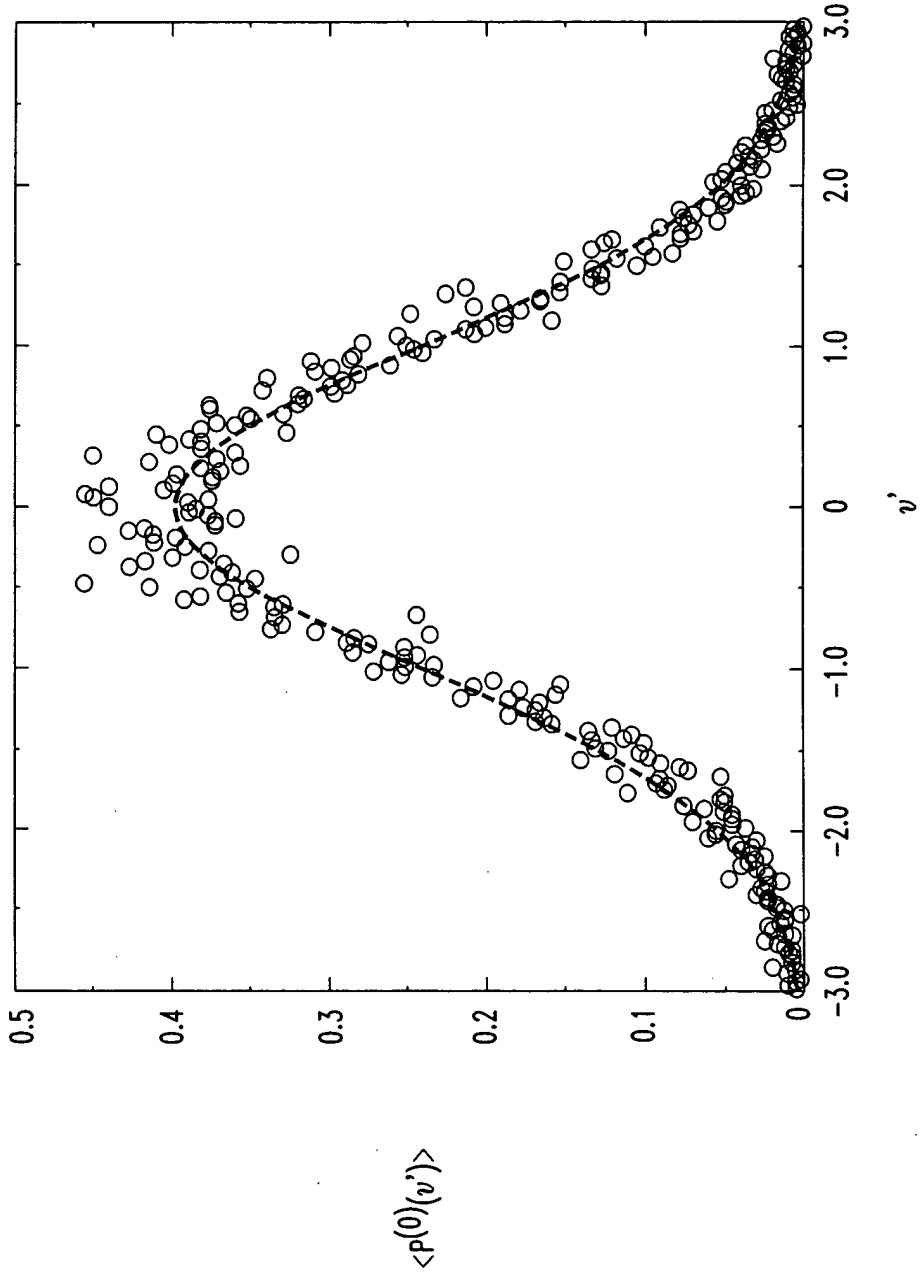



FIG. 10

*FIG. 11*

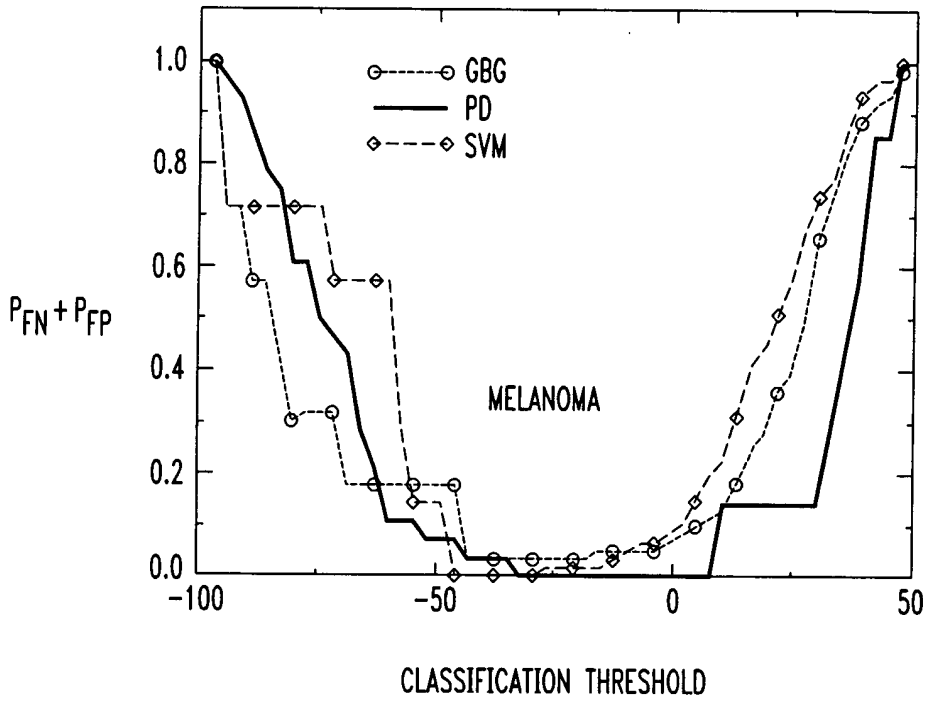

GBG
PD
SVM
MELANOMA
$P_{FN} + P_{FP}$
1.0
0.8
0.6
0.4
0.2
0.0
-100
-50
0
50
CLASSIFICATION THRESHOLD

*FIG. 12*

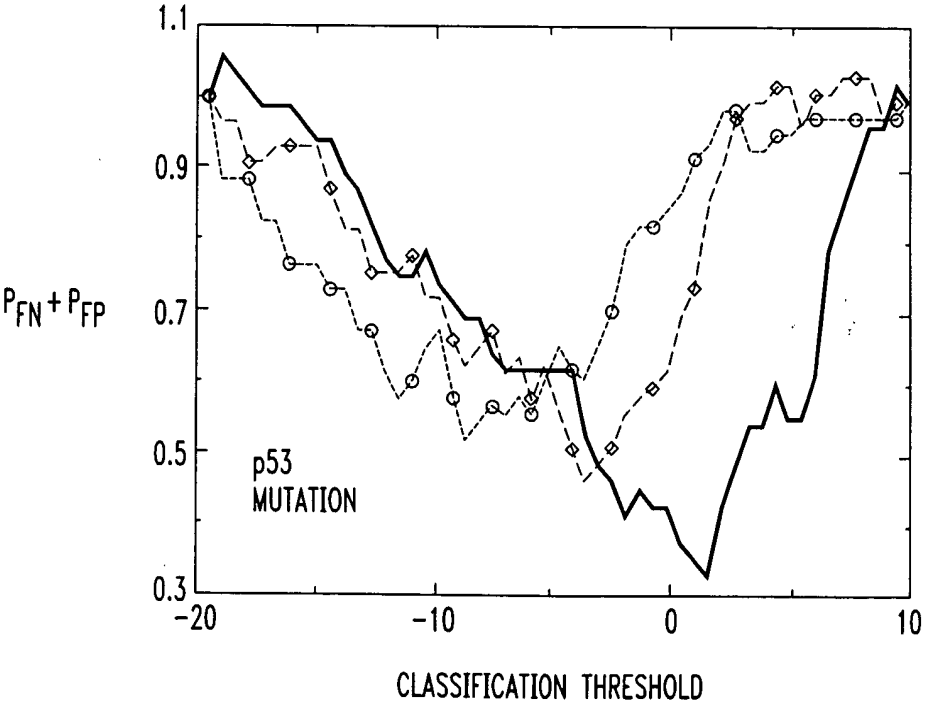

$P_{FN} + P_{FP}$
1.1
0.9
0.7
0.5
0.3
p53
MUTATION
-20
-10
0
10
CLASSIFICATION THRESHOLD

*FIG. 13*

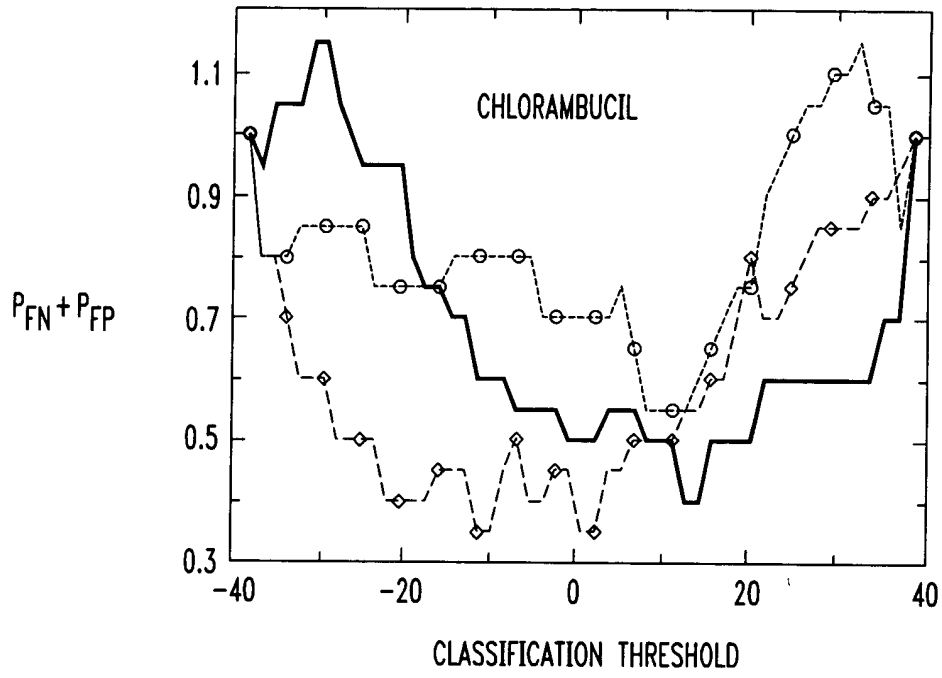

CHLORAMBUCIL
$P_{FN} + P_{FP}$
1.1
0.9
0.7
0.5
0.3
-40
-20
0
20
40
CLASSIFICATION THRESHOLD

*FIG. 14*

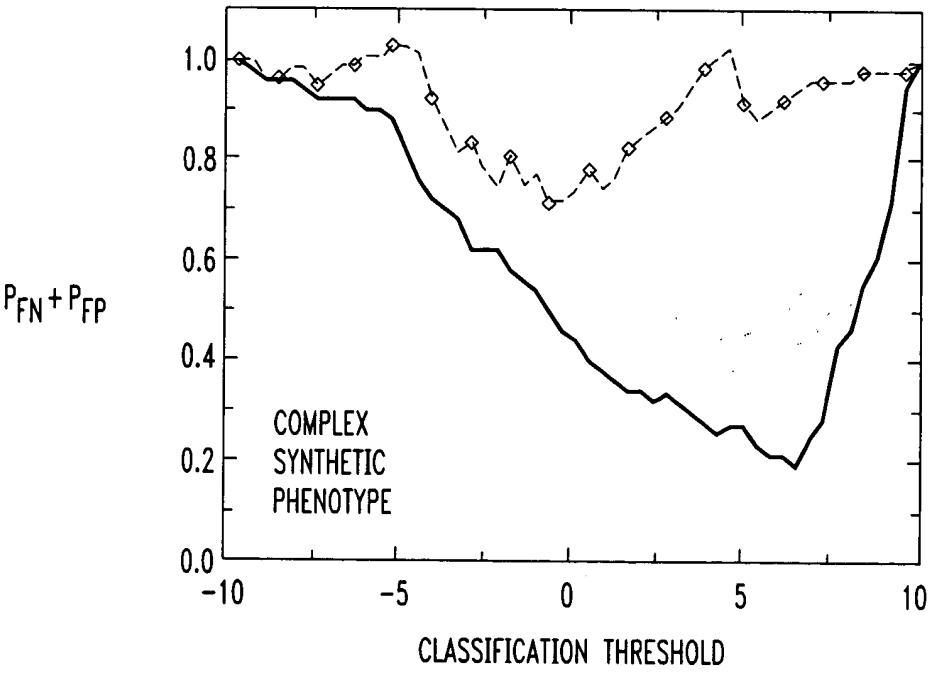
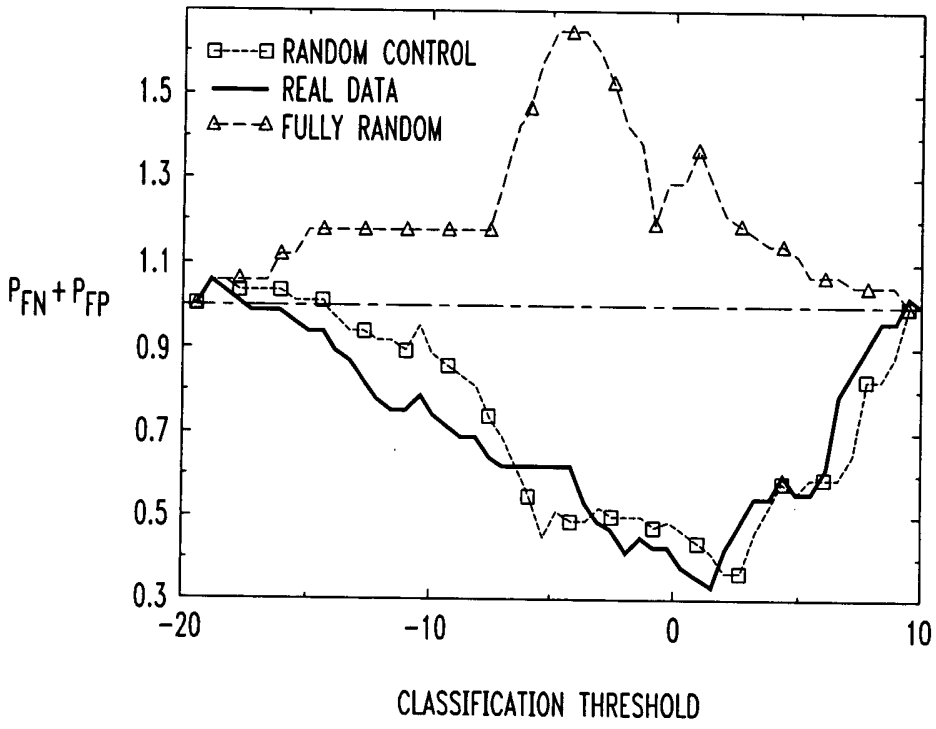

COMPLEX
SYNTHETIC
PHENOTYPE
$P_{FN} + P_{FP}$
1.0
0.8
0.6
0.4
0.2
0.0
-10
-5
0
5
10
CLASSIFICATION THRESHOLD

*FIG. 15*


RANDOM CONTROL
REAL DATA
FULLY RANDOM
1.5
1.3
1.1
0.9
0.7
0.5
0.3
$P_{FN} + P_{FP}$
-20
-10
0
10
CLASSIFICATION THRESHOLD